

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/579,386  
Source: IFWP  
Date Processed by STIC: 05/23/2006

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 05/23/2006

PATENT APPLICATION: US/10/579,386

TIME: 14:30:51

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\05232006\J579386.raw

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3 <110> APPLICANT: OXAGEN LIMITED
4     Jonathon M. TINSLEY
6 <120> TITLE OF INVENTION: Ligand
8 <130> FILE REFERENCE: 117-585 / N.89652C GCW
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/579,386
11 <141> CURRENT FILING DATE: 2006-05-15
13 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/005057
14 <151> PRIOR FILING DATE: 2004-12-02
16 <150> PRIOR APPLICATION NUMBER: GB 0328275.3
17 <151> PRIOR FILING DATE: 2003-12-05
19 <150> PRIOR APPLICATION NUMBER: GB 0403014.4
20 <151> PRIOR FILING DATE: 2004-02-11
22 <150> PRIOR APPLICATION NUMBER: GB 0418568.2
23 <151> PRIOR FILING DATE: 2004-08-19
25 <160> NUMBER OF SEQ ID NOS: 6
27 <170> SOFTWARE: MS Word
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 1531
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (48)..(1118)
38 <400> SEQUENCE: 1
39 aggaagctgc ttcggggggt gagcaaactt tttaaaatgc agaaatt atg atc tac      56
40                                     Met Ile Tyr
41                                     1
43 acc cgt ttc tta aaa ggc agt ctg aag atg gcc aat tac acg ctg gca      104
44 Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr Thr Leu Ala
45     5                10                15
47 cca gag gat gaa tat gat gtc ctc ata gaa ggt gaa ctg gag agc gat      152
48 Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu Glu Ser Asp
49 20                25                30                35
51 gag gca gag caa tgt gac aag tat gac gcc cag gca ctc tca gcc cag      200
52 Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu Ser Ala Gln
53                40                45                50
55 ctg gtg cca tca ctc tgc tct gct gtg ttt gtg atc ggt gtc ctg gac      248
56 Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly Val Leu Asp
57                55                60                65
59 aat ctc ctg gtt gtg ctt atc ctg gta aaa tat aaa gga ctc aaa cgc      296
60 Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly Leu Lys Arg
61                70                75                80
63 gtg gaa aat atc tat ctt cta aac ttg gca gtt tct aac ttg tgt ttc      344

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64	Val	Glu	Asn	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Val	Ser	Asn	Leu	Cys	Phe	
65		85					90				95						
67	ttg	ctt	acc	ctg	ccc	ttc	tgg	gct	cat	gct	ggg	ggc	gat	ccc	atg	tgt	392
68	Leu	Leu	Thr	Leu	Pro	Phe	Trp	Ala	His	Ala	Gly	Gly	Asp	Pro	Met	Cys	
69	100					105					110				115		
71	aaa	att	ctc	att	gga	ctg	tac	ttc	gtg	ggc	ctg	tac	agt	gag	aca	ttt	440
72	Lys	Ile	Leu	Ile	Gly	Leu	Tyr	Phe	Val	Gly	Leu	Tyr	Ser	Glu	Thr	Phe	
73					120					125					130		
75	ttc	aat	tgc	ctt	ctg	act	gtg	caa	agg	tac	cta	gtg	ttt	ttg	cac	aag	488
76	Phe	Asn	Cys	Leu	Leu	Thr	Val	Gln	Arg	Tyr	Leu	Val	Phe	Leu	His	Lys	
77				135				140						145			
79	ggc	aac	ttt	ttc	tca	gcc	agg	agg	agg	gtg	ccc	tgt	ggc	atc	att	aca	536
80	Gly	Asn	Phe	Phe	Ser	Ala	Arg	Arg	Arg	Val	Pro	Cys	Gly	Ile	Ile	Thr	
81		150					155						160				
83	agt	gtc	ctg	gca	tgg	gta	aca	gcc	att	ctg	gcc	act	ttg	cct	gaa	tac	584
84	Ser	Val	Leu	Ala	Trp	Val	Thr	Ala	Ile	Leu	Ala	Thr	Leu	Pro	Glu	Tyr	
85		165				170					175						
87	gtg	gtt	tat	aaa	cct	cag	atg	gaa	gac	cag	aaa	tac	aag	tgt	gca	ttt	632
88	Val	Val	Tyr	Lys	Pro	Gln	Met	Glu	Asp	Gln	Lys	Tyr	Lys	Cys	Ala	Phe	
89	180				185					190					195		
91	agc	aga	act	ccc	ttc	ctg	cca	gct	gat	gag	aca	ttc	tgg	aag	cat	ttt	680
92	Ser	Arg	Thr	Pro	Phe	Leu	Pro	Ala	Asp	Glu	Thr	Phe	Trp	Lys	His	Phe	
93				200						205				210			
95	ctg	act	tta	aaa	atg	aac	att	tcg	gtt	ctt	gtc	ctc	ccc	cta	ttt	att	728
96	Leu	Thr	Leu	Lys	Met	Asn	Ile	Ser	Val	Leu	Val	Leu	Pro	Leu	Phe	Ile	
97				215					220					225			
99	ttt	aca	ttt	ctc	tat	gtg	caa	atg	aga	aaa	aca	cta	agg	ttc	agg	gag	776
100	Phe	Thr	Phe	Leu	Tyr	Val	Gln	Met	Arg	Lys	Thr	Leu	Arg	Phe	Arg	Glu	
101		230					235					240					
103	cag	agg	tat	agc	ctt	ttc	aag	ctt	gtt	ttt	gcc	ata	atg	gta	gtc	ttc	824
104	Gln	Arg	Tyr	Ser	Leu	Phe	Lys	Leu	Val	Phe	Ala	Ile	Met	Val	Val	Phe	
105		245				250					255						
107	ctt	ctg	atg	tgg	gcg	ccc	tac	aat	att	gca	ttt	ttc	ctg	tcc	act	ttc	872
108	Leu	Leu	Met	Trp	Ala	Pro	Tyr	Asn	Ile	Ala	Phe	Phe	Leu	Ser	Thr	Phe	
109	260				265					270				275			
111	aaa	gaa	cac	ttc	tcc	ctg	agt	gac	tgc	aag	agc	agc	tac	aat	ctg	gac	920
112	Lys	Glu	His	Phe	Ser	Leu	Ser	Asp	Cys	Lys	Ser	Ser	Tyr	Asn	Leu	Asp	
113				280						285				290			
115	aaa	agt	gtt	cac	atc	act	aaa	ctc	atc	gcc	acc	acc	cac	tgc	tgc	atc	968
116	Lys	Ser	Val	His	Ile	Thr	Lys	Leu	Ile	Ala	Thr	Thr	His	Cys	Cys	Ile	
117				295					300					305			
119	aac	cct	ctc	ctg	tat	gcg	ttt	ctt	gat	ggg	aca	ttt	agc	aaa	tac	ctc	1016
120	Asn	Pro	Leu	Leu	Tyr	Ala	Phe	Leu	Asp	Gly	Thr	Phe	Ser	Lys	Tyr	Leu	
121		310					315						320				
123	tgc	cgc	tgt	ttc	cat	ctg	cgt	agt	aac	acc	cca	ctt	caa	ccc	agg	ggg	1064
124	Cys	Arg	Cys	Phe	His	Leu	Arg	Ser	Asn	Thr	Pro	Leu	Gln	Pro	Arg	Gly	
125		325				330					335						
127	cag	tct	gca	caa	ggc	aca	tcg	agg	gaa	gaa	cct	gac	cat	tcc	acc	gaa	1112
128	Gln	Ser	Ala	Gln	Gly	Thr	Ser	Arg	Glu	Glu	Pro	Asp	His	Ser	Thr	Glu	

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129 340          345          350          355
131 gtg taa actagcatcc accaaatgca agaagaataa acatggattt tcatctttct      1168
132 Val
135 gcattatttc atgtaaattt tctacacatt tgtatacaaa atcggatata ggaagaaaag      1228
137 ggagaggtga gctaacattt gctaagcact gaatttgtct caggcaccgt gcaaggctct      1288
139 ttacaaacgt gagtccttc gcctcctacc acttgtccat agtgtggata ggactagtct      1348
141 catttctctg agaagaaaac taaggcgcg aaatttgtct aagatcacat aactaggaag      1408
143 tggcagaact gattctccag ccctggtagc atttgctcag agcctacgct tgggccagaa      1468
145 catcaaactc caaacctgg ggacaaacga catgaaataa atgtatttta aaacatctaa      1528
147 aaa                                                                1531
150 <210> SEQ ID NO: 2
151 <211> LENGTH: 356
152 <212> TYPE: PRT
153 <213> ORGANISM: Homo sapiens
155 <400> SEQUENCE: 2
157 Met Ile Tyr Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr
158 1          5          10          15
160 Thr Leu Ala Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu
161          20          25          30
163 Glu Ser Asp Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu
164          35          40          45
166 Ser Ala Gln Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly
167          50          55          60
169 Val Leu Asp Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly
170 65          70          75          80
172 Leu Lys Arg Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn
173          85          90          95
175 Leu Cys Phe Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp
176          100         105         110
178 Pro Met Cys Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser
179          115         120         125
181 Glu Thr Phe Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe
182          130         135         140
184 Leu His Lys Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly
185 145         150         155         160
187 Ile Ile Thr Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu
188          165         170         175
190 Pro Glu Tyr Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys
191          180         185         190
193 Cys Ala Phe Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp
194          195         200         205
196 Lys His Phe Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro
197          210         215         220
199 Leu Phe Ile Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg
200 225         230         235         240
202 Phe Arg Glu Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Ile Met
203          245         250         255
205 Val Val Phe Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu
206          260         265         270

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208 Ser Thr Phe Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr
209          275          280          285
211 Asn Leu Asp Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His
212          290          295          300
214 Cys Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser
216 305          310          315          320
218 Lys Tyr Leu Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln
219          325          330          335
221 Pro Arg Gly Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His
222          340          345          350
224 Ser Thr Glu Val
225          355
228 <210> SEQ ID NO: 3
229 <211> LENGTH: 1771
230 <212> TYPE: DNA
231 <213> ORGANISM: Homo sapiens
234 <220> FEATURE:
235 <221> NAME/KEY: CDS
236 <222> LOCATION: (328)..(1362)
238 <400> SEQUENCE: 3
239 aaaggtcaca gggaaatcaa aggcggggta cagggccaga gggaggagga aacaacttcc      60
241 cggttgcttt cagacgttc agagatcctc tggaggcctg gggagcttt tgagtacttt      120
243 atttcagttg gtccctgagc tcggtgagtg ggcgggtag agccaccagg ggaatcaaca      180
245 gtggtttctc gtgccctca gggtcaggag cagtctgatc aaaaggaggg catccactgt      240
247 ccggggccat tcccacagct cccggatgct ggtctggag gctgcgccct tcccctgcag      300
249 gagctcagcc cagtgggcag tctgaag atg gcc aat tac acg ctg gca cca gag      354
250          Met Ala Asn Tyr Thr Leu Ala Pro Glu
251          1          5
253 gat gaa tat gat gtc ctc ata gaa ggt gaa ctg gag agc gat gag gca      402
254 Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu Glu Ser Asp Glu Ala
255 10          15          20          25
257 gag caa tgt gac aag tat gac gcc cag gca ctc tca gcc cag ctg gtg      450
258 Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu Ser Ala Gln Leu Val
259          30          35          40
261 cca tca ctc tgc tct gct gtg ttt gtg atc ggt gtc ctg gac aat ctc      498
262 Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly Val Leu Asp Asn Leu
263          45          50          55
265 ctg gtt gtg ctt atc ctg gta aaa tat aaa gga ctc aaa cgc gtg gaa      546
266 Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly Leu Lys Arg Val Glu
267          60          65          70
269 aat atc tat ctt cta aac ttg gca gtt tct aac ttg tgt ttc ttg ctt      594
270 Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn Leu Cys Phe Leu Leu
271          75          80          85
273 acc ctg ccc ttc tgg gct cat gct ggg ggc gat ccc atg tgt aaa att      642
274 Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp Pro Met Cys Lys Ile
275 90          95          100          105
277 ctc att gga ctg tac ttc gtg ggc ctg tac agt gag aca ttt ttc aat      690
278 Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser Glu Thr Phe Phe Asn
279          110          115          120

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281	tgc	ctt	ctg	act	gtg	caa	agg	tac	cta	gtg	ttt	ttg	cac	aag	ggc	aac	738
282	Cys	Leu	Leu	Thr	Val	Gln	Arg	Tyr	Leu	Val	Phe	Leu	His	Lys	Gly	Asn	
283				125						130					135		
285	ttt	ttc	tca	gcc	agg	agg	agg	gtg	ccc	tgt	ggc	atc	att	aca	agt	gtc	786
286	Phe	Phe	Ser	Ala	Arg	Arg	Arg	Val	Pro	Cys	Gly	Ile	Ile	Thr	Ser	Val	
287				140					145					150			
289	ctg	gca	tgg	gta	aca	gcc	att	ctg	gcc	act	ttg	cct	gaa	tac	gtg	gtt	834
290	Leu	Ala	Trp	Val	Thr	Ala	Ile	Leu	Ala	Thr	Leu	Pro	Glu	Tyr	Val	Val	
291		155					160					165					
293	tat	aaa	cct	cag	atg	gaa	gac	cag	aaa	tac	aag	tgt	gca	ttt	agc	aga	882
294	Tyr	Lys	Pro	Gln	Met	Glu	Asp	Gln	Lys	Tyr	Lys	Cys	Ala	Phe	Ser	Arg	
295	170					175					180					185	
297	act	ccc	ttc	ctg	cca	gct	gat	gag	aca	ttc	tgg	aag	cat	ttt	ctg	act	930
298	Thr	Pro	Phe	Leu	Pro	Ala	Asp	Glu	Thr	Phe	Trp	Lys	His	Phe	Leu	Thr	
299					190						195				200		
301	tta	aaa	atg	aac	att	tcg	gtt	ctt	gtc	ctc	ccc	cta	ttt	att	ttt	aca	978
302	Leu	Lys	Met	Asn	Ile	Ser	Val	Leu	Val	Leu	Pro	Leu	Phe	Ile	Phe	Thr	
303				205					210					215			
305	ttt	ctc	tat	gtg	caa	atg	aga	aaa	aca	cta	agg	ttc	agg	gag	cag	agg	1026
306	Phe	Leu	Tyr	Val	Gln	Met	Arg	Lys	Thr	Leu	Arg	Phe	Arg	Glu	Gln	Arg	
307			220					225					230				
309	tat	agc	ctt	ttc	aag	ctt	gtt	ttt	gcc	ata	atg	gta	gtc	ttc	ctt	ctg	1074
310	Tyr	Ser	Leu	Phe	Lys	Leu	Val	Phe	Ala	Ile	Met	Val	Val	Phe	Leu	Leu	
311			235				240					245					
313	atg	tgg	gcg	ccc	tac	aat	att	gca	ttt	ttc	ctg	tcc	act	ttc	aaa	gaa	1122
314	Met	Trp	Ala	Pro	Tyr	Asn	Ile	Ala	Phe	Phe	Leu	Ser	Thr	Phe	Lys	Glu	
315	250					255					260				265		
317	cac	ttc	tcc	ctg	agt	gac	tgc	aag	agc	agc	tac	aat	ctg	gac	aaa	agt	1170
318	His	Phe	Ser	Leu	Ser	Asp	Cys	Lys	Ser	Ser	Tyr	Asn	Leu	Asp	Lys	Ser	
319				270						275					280		
321	gtt	cac	atc	act	aaa	ctc	atc	gcc	acc	cac	tgc	tgc	atc	aac	cct		1218
322	Val	His	Ile	Thr	Lys	Leu	Ile	Ala	Thr	Thr	His	Cys	Cys	Ile	Asn	Pro	
323				285					290					295			
325	ctc	ctg	tat	gcg	ttt	ctt	gat	ggg	aca	ttt	agc	aaa	tac	ctc	tgc	cgc	1266
326	Leu	Leu	Tyr	Ala	Phe	Leu	Asp	Gly	Thr	Phe	Ser	Lys	Tyr	Leu	Cys	Arg	
327			300					305					310				
329	tgt	ttc	cat	ctg	cgt	agt	aac	acc	cca	ctt	caa	ccc	agg	ggg	cag	tct	1314
330	Cys	Phe	His	Leu	Arg	Ser	Asn	Thr	Pro	Leu	Gln	Pro	Arg	Gly	Gln	Ser	
331			315				320					325					
333	gca	caa	ggc	aca	tcg	agg	gaa	gaa	cct	gac	cat	tcc	acc	gaa	gtg	taa	1362
334	Ala	Gln	Gly	Thr	Ser	Arg	Glu	Glu	Pro	Asp	His	Ser	Thr	Glu	Val		
335	330					335					340						
337	actagcatcc	accaa	atgca	aga	agaataa	acatggattt	tcatctttct	gcattatttc									1422
339	atgtaaat	ttt	tctacacatt	tgtatacaaaa	atcggataca	ggaagaaaag	ggagaggtga										1482
341	gctaaca	attt	gctaagcact	gaattt	gtct	caggcaccgt	gcaaggctct	ttacaaacgt									1542
343	gagctc	cttc	gcctcctacc	actt	gtccat	agtgtggata	ggactagtct	caattctctg									1602
345	agaagaaa	aac	taaggcg	cgg	aaattt	gtct	aagatcacat	aactaggaag	tggcagaact								1662
347	gattctccag	ccctg	gtagc	attt	gtctag	agcctacgct	tggccagaa	catcaaactc									1722
349	caaaccct	g	ggacaaa	cga	catgaaa	ataa	atgtatttta	aaacatcta									1771

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L:10 M:270 C: Current Application Number differs, Wrong Format